

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/565,831  
Source: STW4  
Date Processed by STIC: 1-30-06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , **EFS Submission User Manual - ePAVE**)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

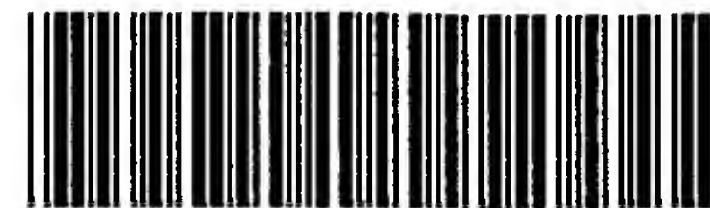
### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/565,831

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2        Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3        Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
  
- 4        Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
  
- 5        Variable Length     Sequence(s)        contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6        PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7        Skipped Sequences  
    (OLD RULES)     Sequence(s)        missing. If intentional, please insert the following lines for **each** skipped sequence:  
                                   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                   (i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                   (xi)  SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                   This sequence is intentionally skipped  
  
                                   Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8        Skipped Sequences  
    (NEW RULES)     Sequence(s)        missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                                   <210> sequence id number  
                                   <400> sequence id number  
                                   000
  
- 9        Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                                   Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                                   In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
- 10        Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
  
- 11 ✓ Use of <220>     Sequence(s) 1-16 missing the <220> "Feature"  
                                   Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                                   (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12        PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13        Misuse of n/Xaa     "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWP

## RAW SEQUENCE LISTING

DATE: 01/30/2006

PATENT APPLICATION: US/10/565,831

TIME: 16:02:38

Input Set : A:\Q92863 Sequence Listing.txt

Output Set: N:\CRF4\01302006\J565831.raw

3 <110> APPLICANT: ONO PHARMACEUTICAL CO., LTD.  
 4 Junya TOGUCHIDA  
 6 <120> TITLE OF INVENTION: REMEDY FOR CARTILAGE-RELATED DISEASES  
 8 <130> FILE REFERENCE: Q92863  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/565,831  
 C--> 10 <141> CURRENT FILING DATE: 2006-01-25  
 10 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/010890  
 11 <151> PRIOR FILING DATE: 2004-07-23  
 13 <150> PRIOR APPLICATION NUMBER: JP 2003-280191  
 14 <151> PRIOR FILING DATE: 2003-07-25  
 16 <160> NUMBER OF SEQ ID NOS: 16  
 18 <170> SOFTWARE: PatentIn version 3.1

Does Not Comply  
 Corrected Diskette Needed

(Pg. 1-3) ↗

## ERRORED SEQUENCES

20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 36  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Mus musculus  
 24 ~~<220>~~ OTHER INFORMATION: Antisense oligonucleotide  
 E--> 25 <400> SEQUENCE: 1  
 26 acagtaccct ggcacctggt gttttattag ccttgg  
 28 <210> SEQ ID NO: 2  
 29 <211> LENGTH: 36  
 30 <212> TYPE: DNA  
 31 ~~<213>~~ ORGANISM: Mus musculus  
 32 ~~<223>~~ OTHER INFORMATION: Antisense oligonucleotide  
 E--> 33 <400> SEQUENCE: 2  
 34 aaagattgtg aaaggcaagg agcatatggc gaaggt  
 36 <210> SEQ ID NO: 3  
 37 <211> LENGTH: 36  
 38 <212> TYPE: DNA  
 39 ~~<213>~~ ORGANISM: Mus musculus  
 40 ~~<223>~~ OTHER INFORMATION: Antisense oligonucleotide  
 E--> 41 <400> SEQUENCE: 3  
 42 cagcagataa acccagggat ccaagatctg gttcag  
 44 <210> SEQ ID NO: 4  
 45 <211> LENGTH: 36  
 46 <212> TYPE: DNA  
 47 ~~<213>~~ ORGANISM: Mus musculus  
 48 ~~<223>~~ OTHER INFORMATION: Antisense oligonucleotide  
 E--> 49 <400> SEQUENCE: 4

← pls insert (220)  
 whenever (221),  
 (222), (223) is  
 present.  
 36

pls see  
 item #  
 36

same error ↗

same error ↗

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/565,831

DATE: 01/30/2006

TIME: 16:02:38

Input Set : A:\Q92863 Sequence Listing.txt

Output Set: N:\CRF4\01302006\J565831.raw

50 ggaggagtct gaggtctcgg aaattcgcaa agttct 36

52 <210> SEQ ID NO: 5

53 <211> LENGTH: 21

54 <212> TYPE: DNA

55 <213> ORGANISM: Homo sapiens

56 <223> OTHER INFORMATION: PCR primer oligonucleotide

OK E--> 57 <400> SEQUENCE: 5

58 acctggtgtt ttattagcct t

60 <210> SEQ ID NO: 6

61 <211> LENGTH: 21

62 <212> TYPE: DNA

63 <213> ORGANISM: Homo sapiens

64 <223> OTHER INFORMATION: PCR primer oligonucleotide

OK E--> 65 <400> SEQUENCE: 6

66 ggccgctgca gggagttaga g

68 <210> SEQ ID NO: 7

69 <211> LENGTH: 20

70 <212> TYPE: DNA

71 <213> ORGANISM: Homo sapiens

72 <223> OTHER INFORMATION: PCR primer oligonucleotide

OK E--> 73 <400> SEQUENCE: 7

74 cgtgtacctt tttcgctttc

76 <210> SEQ ID NO: 8

77 <211> LENGTH: 20

78 <212> TYPE: DNA

79 <213> ORGANISM: Homo sapiens

80 <223> OTHER INFORMATION: PCR primer oligonucleotide

OK E--> 81 <400> SEQUENCE: 8

82 gaggtccac ttttccttta

84 <210> SEQ ID NO: 9

85 <211> LENGTH: 21

86 <212> TYPE: DNA

87 <213> ORGANISM: Homo sapiens

88 <223> OTHER INFORMATION: PCR primer oligonucleotide

OK E--> 89 <400> SEQUENCE: 9

90 catcgactgg accaccaacg t

92 <210> SEQ ID NO: 10

93 <211> LENGTH: 21

94 <212> TYPE: DNA

95 <213> ORGANISM: Homo sapiens

96 <223> OTHER INFORMATION: PCR primer oligonucleotide

OK E--> 97 <400> SEQUENCE: 10

98 tctcctttaa ctcccgggag a

100 <210> SEQ ID NO: 11

101 <211> LENGTH: 22

102 <212> TYPE: DNA

103 <213> ORGANISM: Homo sapiens

104 <223> OTHER INFORMATION: PCR primer oligonucleotide

OK E--> 105 <400> SEQUENCE: 11

Same  
errors

## RAW SEQUENCE LISTING

DATE: 01/30/2006

PATENT APPLICATION: US/10/565,831

TIME: 16:02:38

Input Set : A:\Q92863 Sequence Listing.txt

Output Set: N:\CRF4\01302006\J565831.raw

106 cctgggttta tctgctgcta ag 22

108 <210> SEQ ID NO: 12

109 <211> LENGTH: 22

110 <212> TYPE: DNA

111 <213> ORGANISM: Homo sapiens

112 <223> OTHER INFORMATION: PCR primer oligonucleotide

OK E-> 113 <400> SEQUENCE: 12

114 ctcggtgtgt ttaatggcaa gg

116 <210> SEQ ID NO: 13

117 <211> LENGTH: 22

118 <212> TYPE: DNA

119 <213> ORGANISM: Homo sapiens

120 <223> OTHER INFORMATION: PCR primer oligonucleotide

OK E-> 121 <400> SEQUENCE: 13

122 cctgggttta tctgctgcta ag

124 <210> SEQ ID NO: 14

125 <211> LENGTH: 22

126 <212> TYPE: DNA

127 <213> ORGANISM: Homo sapiens

128 <223> OTHER INFORMATION: PCR primer oligonucleotide

OK E-> 129 <400> SEQUENCE: 14

130 ctctggcaaa gactcaaaat gc

132 <210> SEQ ID NO: 15

133 <211> LENGTH: 20

134 <212> TYPE: DNA

135 <213> ORGANISM: Homo sapiens

136 <223> OTHER INFORMATION: PCR primer oligonucleotide

OK E-> 137 <400> SEQUENCE: 15

138 aagagaggta tcctgaccct

140 <210> SEQ ID NO: 16

141 <211> LENGTH: 20

142 <212> TYPE: DNA

143 <213> ORGANISM: Homo sapiens

144 <223> OTHER INFORMATION: PCR primer oligonucleotide

OK E-> 145 <400> SEQUENCE: 16

146 tacatggctg ggggtgtgaa

22

22

22

20

20

Same  
errors



## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/565,831

DATE: 01/30/2006

TIME: 16:02:39

Input Set : A:\Q92863 Sequence Listing.txt

Output Set: N:\CRF4\01302006\J565831.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:25 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:1  
L:25 M:283 W: Missing Blank Line separator, <400> field identifier  
L:33 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:2  
L:33 M:283 W: Missing Blank Line separator, <400> field identifier  
L:41 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:3  
L:41 M:283 W: Missing Blank Line separator, <400> field identifier  
L:49 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:4  
L:49 M:283 W: Missing Blank Line separator, <400> field identifier  
L:57 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:5  
L:57 M:283 W: Missing Blank Line separator, <400> field identifier  
L:65 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:6  
L:65 M:283 W: Missing Blank Line separator, <400> field identifier  
L:73 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:7  
L:73 M:283 W: Missing Blank Line separator, <400> field identifier  
L:81 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:8  
L:81 M:283 W: Missing Blank Line separator, <400> field identifier  
L:89 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:9  
L:89 M:283 W: Missing Blank Line separator, <400> field identifier  
L:97 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:10  
L:97 M:283 W: Missing Blank Line separator, <400> field identifier  
L:105 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:11  
L:105 M:283 W: Missing Blank Line separator, <400> field identifier  
L:113 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:12  
L:113 M:283 W: Missing Blank Line separator, <400> field identifier  
L:121 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:13  
L:121 M:283 W: Missing Blank Line separator, <400> field identifier  
L:129 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:14  
L:129 M:283 W: Missing Blank Line separator, <400> field identifier  
L:137 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:15  
L:137 M:283 W: Missing Blank Line separator, <400> field identifier  
L:145 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:16  
L:145 M:283 W: Missing Blank Line separator, <400> field identifier